

PS Example 1; Page 42; 74PP; English.

XX WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation -

XX Claim 8; Page 58; 74PP; English.

CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

CC Sequence 31 AA;

Query Match	Score	DB	Length	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
31; Conservative	100.0%	23	31	100.0%	1.9e-17	0	0	0

QY 1 KPVSLSYRPCPCRFGGGLKWIQEYLEKALN 31

Db 1 KPVSLSYRPCPCRFGGGLKWIQEYLEKALN 31

RESULT 2

ID AAB47693

ID AAB47693 standard; peptide; 31 AA.

XX AAB47693;

AC AAB47693;

DT 30-JAN-2002 (first entry)

XX DE SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.

KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

KW Synthetic.

OS WO200176615-A2.

XX PN WO200176615-A2.

PD 18-OCT-2001.

PR 12-APR-2001; 2001WO-CA00540.

XX 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

PI Cashman J, Clark-Lewis I;

XX WPI; 2002-025882/03.

DR CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation -

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation -

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CC used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX SO Sequence 31 AA:

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	31; Conservative	100.0%; Pred. No.	1.9e-17;	31;	0;	0;
Oy	1	KPVSLSYRCPCRCRFFGGGLKWIQEYLEKALN	31			
Db	1	KPVSLSYRCPCRCRFFGGGLKWIQEYLEKALN	31			

RESULT 4

AAB47700

ID AAB47700 standard; peptide; 31 AA.

XX AC AAB47700;

XX DT 30-JAN-2002 (first entry)

XX DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic acid.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX FH Key

FT Location/Qualifiers

FT Modified-site 24..28 /note= "Joined by side chain cyclization using lactam formation"

XX PN WO200176615-A2.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

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XX PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ; Cashman J, Clark-Lewis I;

XX DR WPI; 2002-025882/03.

XX PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

XX PS Example 1; Page 43; 74pp; English.

XX CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These Peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing

CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX SO Sequence 31 AA:

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	31; Conservative	100.0%; Pred. No.	1.9e-17;	31;	0;	0;
Oy	1	KPVSLSYRCPCRCRFFGGGLKWIQEYLEKALN	31			
Db	1	KPVSLSYRCPCRCRFFGGGLKWIQEYLEKALN	31			

RESULT 5

AAB47701

ID AAB47701 standard; peptide; 31 AA.

XX AC AAB47701;

XX DT 30-JAN-2002 (first entry)

XX DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic acid.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX FH Key

FT Location/Qualifiers

FT Modified-site 20..24 /note= "Joined by side chain cyclization using lactam formation"

XX PN WO200176615-A2.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

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XX PS Example 1; Page 43; 74pp; English.

XX CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These Peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing

CC sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA:

Query	Match	Score	DB	Length	Indels	Gaps
Db	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN	175	23	31	0	0

RESULT 6

AAB47702

ID AAB47702 standard; peptide; 31 AA.

XX

AC AAB47702;

XX

DT 30-JAN-2002 (first entry)

XX

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX

FH Key

FT Location/Qualifiers

FT Modified-site 24..28

FT /note= "joined by side chain cyclization using lactam formation"

FT Modified-site 31

FT /note= "C-terminal amide"

FT WO200176615-A2.

PN XX

PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

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XX DR WPI; 2002-025882/03.

XX PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation -

XX PS Example 1; Page 43; 74pp; English.

CC sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX Sequence 31 AA:

Query	Match	Score	DB	Length	Indels	Gaps
Db	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN	175	23	31	0	0

RESULT 7

AAB47703

ID AAB47703 standard; peptide; 31 AA.

XX

AC AAB47703;

XX

DT 30-JAN-2002 (first entry)

XX

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX

FH Key

FT Location/Qualifiers

FT Modified-site 20..24

FT /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31

FT /note= "C-terminal amide"

FT WO200176615-A2.

PN XX

PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

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PI Cashman J, Clark-Lewis I;

XX DR WPI; 2002-025882/03.

XX PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation -

XX PS Example 1; Page 43; 74pp; English.

CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing

CC sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the CC agonist peptides to the cells prior to or during exposure of the CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly CC in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

CC or peripheral blood stem cell transplantation, or an autoimmune disease.

XX SQ Sequence 31 AA;

Query	Match	Score	DB	Length
QY	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31	100.0%	23	31;
Db	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31	100.0%	23	31;

Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

ID AAB47706 standard; peptide: 31 AA.

XX AC AAB47706;

XX DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-c9/c11-cyclic acid.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease; KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 9..11

XX PN WO200176615-A2.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

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PI Cashman J, Clark-Lewis I;

XX DR WPI; 2002-025882/03.

XX PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents; are useful for bone marrow or peripheral blood stem cell transplantation

XX Example 1; Page 44; 74pp; English.

PS The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly

CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

XX SQ Sequence 31 AA;

Query	Match	Score	DB	Length
QY	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31	100.0%	23	31;
Db	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31	100.0%	23	31;

Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

ID AAB47707 standard; peptide: 31 AA.

XX AC AAB47707;

XX DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-c9/c11-cyclic amide.

XX HAematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease; KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 9..11

FT Modified-site 31 /note= "C-terminal amide"

XX PN WO200176615-A2.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

XX PR 12-APR-2000; 2000CA-2305036.

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PI Cashman J, Clark-Lewis I;

XX DR WPI; 2002-025882/03.

XX PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

XX Example 1; Page 44; 74pp; English.

PS The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the hematopoietic cells to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly

CC in a patient with cancer requiring autologous or allogenic bone marrow
 CC or peripheral blood stem cell transplantation, or an autoimmune disease.
 XX

SQ Sequence 31 AA;

Query Match 1 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;

Db 1 KPVSLSYRCPCRFFGGGLKWIQEYLEKALN 31

RESULT 10

AAB47714 standard; peptide; 31 AA.

ID AAB47714

XX AAB47714;

AC

XX DT 30-JAN-2002 (first entry)

XX DE SDF-1(1-14) - (G)4 - SDF-1(55-67) acid.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

KW OS Synthetic.

XX PN WO200176615-A2.

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XX DR WPI; 2002-025882/03.

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation

PT Example 1; Page 47; 74pp; English.

XX PS The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

CC Sequence 31 AA;

XX SQ Sequence 31 AA;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQEYLEKALN 31

1 KPVSLSYRCPCRFFGGGLKWIQEYLEKALN 31

RESULT 11

AAB47715 standard; peptide; 31 AA.

ID AAB47715

XX AC AAB47715;

XX DT 30-JAN-2002 (first entry)

XX DE SDF-1(1-14) - (G)4 - SDF-1(55-67) amide.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

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XX PD 18-OCT-2001.

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CC Sequence 31 AA;

XX SQ Sequence 31 AA;

Query Match 1 100.0%; Score 175; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-17; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFFGGGLKWIQEYLEKALN 31

Db 1 |||KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 12

AAB47716 standard; peptide; 31 AA.

ID AAB47716

XX AC AAB47716;

XX DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 24..28 /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

XX PN WO200176615-A2.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-CA00540.

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XX SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 |||KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 13

AAB47717 standard; peptide; 31 AA.

ID AAB47717

XX AC AAB47717;

XX DT 30-JAN-2002 (first entry)

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 20..24 /note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31 /note= "C-terminal amide"

XX PN WO200176615-A2.

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XX SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Db 1 ||||| KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 12

AAB47716

ID AAB47716 standard; peptide; 31 AA.

XX

AC AAB47716;

XX

DT 30-JAN-2002 (first entry)

XX

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-E24/K28-cyclic amide.

XX

KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;

KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;

KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;

KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 24..28

/note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31

/note= "C-terminal amide"

XX

PN WO200176615-A2.

XX

PD 18-OCT-2001.

XX

PF 12-APR-2001; 2001WO-CA00540.

XX

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX

PI Salari H, Marzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

PI Cashman J, Clark-Lewis I;

XX

DR WPI; 2002-025882/03.

XX

PT CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or

PT peripheral blood stem cell transplantation

XX

PS Example 1; Page 47; 74PP; English.

XX

CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

CC

SQ Sequence 31 AA;

Db 1 ||||| KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 13

AAB47717

ID AAB47717 standard; peptide; 31 AA.

XX

AC AAB47717;

XX

DT 30-JAN-2002 (first entry)

XX

DE SDF-1(1-14) - (G)4 - SDF-1(55-67)-K20/E24-cyclic amide.

XX

KW Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;

KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;

KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;

KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 20..24

/note= "Joined by side chain cyclization using lactam formation"

FT Modified-site 31

/note= "C-terminal amide"

XX

PN WO200176615-A2.

XX

PD 18-OCT-2001.

XX

PF 12-APR-2001; 2001WO-CA00540.

XX

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

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XX

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PI Cashman J, Clark-Lewis I;

XX

DR WPI; 2002-025882/03.

XX

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XX

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CC The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or an autoimmune disease.

CC

SQ Sequence 31 AA;

Query Match 100.0%; Score 175; DB 23; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Thu Oct 9 16:38:59 2003

us-09-835-107a-11.rag

Page 9

XX
SQ Sequence 31 AA;
Query Match 98.3%; Score 172; DB 23; Length 31;
Best Local Similarity 96.8%; Pred. No. 5.1e-17;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPVSLISYRCPCRCFFGGGLKWIQEYLEKALN 31
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 KPVSLISYRCPCRCFFGGGLKWIQDYLEKALN 31

Search completed: October 9, 2003, 09:19:01
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:42 ; Search time 39 Seconds
 (without alignments)
 75.442 Million cell updates/sec

Title: US-09-835-107a-11

Perfect score: 175

Sequence: 1 KPVSLSYRCPCRFGGGGKKWIEYELKALN 31

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	2 A53497	pre-B-cell growth-stimulating factor precursor - mouse
2	117	66.9	89	2 I53416	C;Species: Mus musculus (house mouse)
3	117	66.9	93	2 G01540	C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
4	117	66.9	93	2 I81182	C;Accession: A53497; 159582
5	61	34.9	1084	2 T08583	R; Nagasawa, T.; Kikutani, H.; Kishimoto, T.
6	61	34.9	1088	2 H84604	Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
7	60.5	34.6	974	2 T10797	A;Title: Molecular cloning and structure of a Pre-B-cell growth-stimulating factor.
8	58	33.1	469	2 C83345	A;Reference number: A53497; MUID:94181581; PMID:8134392
9	58	33.1	1081	2 T52028	A;Status: preliminary
10	56	32.0	233	2 T35594	A;Molecule type: mRNA
11	54	30.9	398	2 T52311	A;Residues: 1-89 <NAG>
12	53	30.3	454	2 C64104	A;Cross-references: GB:LL12029; NID:9393179; PID:AAA40100.1; PID:g393180
13	53	30.3	470	2 T46814	C;Genetics:
14	53	30.3	470	2 B95419	A;Gene: SDF-1-alpha
15	50	28.6	202	2 AT3489	C;Superfamily: beta-thromboglobulin
16	50	28.6	588	2 S34786	C;Keywords: cytokine
17	50	28.6	685	2 T10800	
18	49.5	28.3	170	2 B85359	Query Match
19	49.5	28.3	577	2 I50731	Best Local Similarity 66.9%; Score 117; DB 2; Length 89;
20	49	28.0	386	2 C81419	Matches 27; Conservative 40.3%; Pred. No. 4.8e-09; Mismatches 4; Indels 36; Gaps 1;
21	49	28.0	508	2 F87198	QY 1 KPVSLSYRCPCRFEGG-
22	49	28.0	517	2 A70793	Db 22 KPVSLSYRCPCRFEGG-
23	49	28.0	556	1 A53376	-GGLKWIQE 24
24	49	28.0	557	1 A25493	QY 25 YLEKALN 31
25	49	28.0	1722	2 A88470	Db 82 YLEKALN 88
26	48	27.4	189	2 D69389	RESULT 2
27	48	27.4	309	1 S34198	I53416
28	48	27.4	331	1 LNMSER	interleukin-8 homolog - mouse
29	48	27.4	383	2 C90136	C;Species: Mus sp. (mouse)

gene 13 protein - probable membrane transporter, AcrB/hemeotic protein 1 hypothetical prote endo-1,4-beta glucosidase protein SN isopenicillin N epitransforming growth phosphatidylcholin probable membrane hypothetical prote Similar to disease hypothetical prote succinate dehydrogenase DNA prima

ALIGNMENTS

RESULT 1

A53497

pre-B-cell growth-stimulating factor precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000

C;Accession: A53497; 159582

R; Nagasawa, T.; Kikutani, H.; Kishimoto, T.

Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A;Title: Molecular cloning and structure of a Pre-B-cell growth-stimulating factor.

A;Reference number: A53497; MUID:94181581; PMID:8134392

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-89 <NAG>

A;Cross-references: GB:D21072; NID:9413905; PIDN:BAA04648.1; PID:g468457

R; Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.

Science 261, 600-603, 1993

A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins

A;Reference number: I59582; MUID:93342488; PMID:8342023

A;Accession: I59582

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-89 <RES>

A;Cross-references: GB:LL12029; NID:9393179; PID:AAA40100.1; PID:g393180

C;Genetics:

A;Gene: SDF-1-alpha

C;Superfamily: beta-thromboglobulin

C;Keywords: cytokine

Query Match

Best Local Similarity 66.9%; Score 117; DB 2; Length 89;

Matches 27; Conservative 40.3%; Pred. No. 4.8e-09; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-

Db 22 KPVSLSYRCPCRFEGG-

-GGLKWIQE 24

QY 25 YLEKALN 31

Db 82 YLEKALN 88

RESULT 2

I53416

interleukin-8 homolog - mouse

C;Species: Mus sp. (mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C;Accession: I53416

R; Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.

Exp. Cell Res. 215, 284-293, 1994

A;Title: Molecular cloning of TPARI, a gene whose expression is repressed by the tumor

A;Reference number: I53416; MUID:95073497; PMID:7982471

A;Accession: I53416
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89 <RES>
A;Cross-references: GB:S74318; NID:g786393; PIDN:AAB32650.1; PID:g786394
C;Genetics:
A;Gene: TPARI
C;Superfamily: beta-thromboglobulin

Query Match 66.9%; Score 117; DB 2; Length 89;
Best Local Similarity 40.3%; Pred. No. 4.8e-09; Mismatches 4; Indels 36; Gaps 1;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGIKWIE 24
Db 22 KPVSLSYRCPCRFESHTIARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81

QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 3

G01540 cytokine SDF-1-beta - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C;Accession: G01540
R;Spotila, L.D.
Submitted to the EMBL Data Library, October 1994
A;Reference number: G07697
A;Accession: G01540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-93 <SPO>
A;Cross-references: EMBL:U16752; NID:g1272194; PID:g571508
C;Superfamily: beta-thromboglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;
Best Local Similarity 40.3%; Pred. No. 5e-09; Mismatches 4; Indels 36; Gaps 1;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGIKWIE 24
Db 22 KPVSLSYRCPCRFESHTIARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81

QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 4

I81182 cytokine - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I81182
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I81182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-93 <RES>
A;Cross-references: GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182
C;Genetics:
A;Gene: SDF-1-beta
C;Superfamily: beta-thromboglobulin

Query Match 66.9%; Score 117; DB 2; Length 93;
Best Local Similarity 40.3%; Pred. No. 5e-09; Mismatches 4; Indels 36; Gaps 1;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFEGG-----GGIKWIE 24
Db 22 KPVSLSYRCPCRFESHTIARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81

QY 25 YLEKALN 31
Db 82 YLEKALN 88

RESULT 5

T08583 cellulose synthase (EC 2.4.1.-) catalytic chain - Arabidopsis thaliana
N;Alternate names: protein T22F8.250
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T08583; T09014
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;
submitted to the Protein Sequence Database, May 1999
A;Reference number: 216442
A;Accession: T08583
A;Molecule type: DNA
A;Residues: 1-1084 <BEV>
A;Cross-references: EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.250
A;Experimental source: cultivar Columbia; BAC clone T22F8
R;Arioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wittke, W.; Herth, W.; Camilleri, C.
Science 279, 717-720, 1998
A;Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A;Reference number: Z13745; MUID:98111412; PMID:9445479
A;Accession: T09014
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1084 <ARI>
A;Cross-references: EMBL:AF027173; NID:g2827140; PIDN: AAC39335.1; PID:g2827141
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: AtSP:T22F8.250; Ath-A
A;Map Position: 4
A;Introns: 27/3; 156/3; 191/1; 254/2; 343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3
C;Keywords: cell wall synthesis; glycosyltransferase; hexosyltransferase

Query Match 34.9%; Score 61; DB 2; Length 1084;
Best Local Similarity 43.5%; Pred. No. 2.6; Mismatches 8; Indels 0; Gaps 0;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRFGGGLKWIQE 25
Db 833 IFLSRHCPPIWYGYGGGLKWLRF 855

RESULT 6

H84604 probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84604
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, J.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, S.;
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84604
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1088 <STO>
A;Cross-references: GB:AE002093; NID:g4417271; PIDN:AAD20396.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g21770
A;Map position: 2

Query Match 34.9%; Score 61; DB 2; Length 1088;
Best Local Similarity 43.5%; Pred. No. 2.6; Mismatches 8; Indels 36; Gaps 1;

Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 3 VSLSYRPCRFFGGGLKWIQEY 25
 C;Species: Gossypium hirsutum (upland cotton)
 R;Joshi, C.
 Db 837 IFLSRHCPINVGYGGGLKWLRF 859
 Submitted to the EMBL Data Library, May 1998
 A;Reference number: Z25890
 A;Accession: T52028
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1081 <JOS>
 A;Cross-references: EMBL:AF062485; PIDN:AAC29067.1

cellulose synthase (EC 2.4.1.-) catalytic chain ccelA - upland cotton
 C;Species: Gossypium hirsutum (upland cotton)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T10797
 R;Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delmer, D.P.; Stalker, D.M.
 PROC. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996
 A;Title: Higher plants contain homologs of the bacterial ccelA genes encoding the catalyst
 A;Reference number: Z17152; MUID:97057296; PMID:8901635
 A;Accession: T10797
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-974 <PEA>
 A;Cross-references: EMBL:U58283; NID:g1706955; PIDN:AAB37766.1; PID:g1706956
 A;Experimental source: strain Acala SJ-2; fiber
 C;Genetics:
 A;Gene: celA
 C;Function:
 A;Description: involved in the synthesis of cellulose
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 34.6%; Score 60.5; DB 2; Length 974;
 Best Local Similarity 54.5%; Pred. No. 2.8;
 Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Pseudomonas aeruginosa PAO1
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bidwell, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: C83345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-469 <STO>
 A;Cross-references: GB:AE004668; GB:AE004091; NID:99948446; PIDN:AAG05801.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA2413

RESULT 8

Query Match 34.6%; Score 60.5; DB 2; Length 974;
 Best Local Similarity 54.5%; Pred. No. 2.8;
 Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Pseudomonas aeruginosa PAO1
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: C83345
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bidwell, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: C83345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-469 <STO>
 A;Cross-references: GB:AE004668; GB:AE004091; NID:99948446; PIDN:AAG05801.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA2413

Query Match 33.1%; Score 58; DB 2; Length 469;
 Best Local Similarity 43.3%; Pred. No. 3.2;
 Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PVLSYRPCRFFGGGLKWIQEYLEKALL 31
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
 A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
 C;Genetics:
 A;Gene: cefD

RESULT 9

Query Match 33.1%; Score 58; DB 2; Length 469;
 Best Local Similarity 43.3%; Pred. No. 3.2;
 Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PVLSYRPCRFFGGGLKWIQEYLEKALL 31
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 8 RPCRFFGGGLKWI 22
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000

Db 205 RIPCDFYAGSGHKWL 219

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 205 RIPCDFYAGSGHKWL 219

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
 A;Accession: T35594
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
 A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
 C;Genetics:
 A;Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 831 IFLSRHCPINVGYGGGLKWL 851

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
 A;Accession: T35594
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
 A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
 C;Genetics:
 A;Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 831 IFLSRHCPINVGYGGGLKWL 851

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
 A;Accession: T35594
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
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 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
 A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
 C;Genetics:
 A;Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 831 IFLSRHCPINVGYGGGLKWL 851

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
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Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
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 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
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 C;Genetics:
 A;Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 831 IFLSRHCPINVGYGGGLKWL 851

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
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Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
 A;Accession: T35594
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
 C;Accession: T52311
 R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
 J. Bacteriol. 172, 3952-3958, 1990
 A;Title: The beta-lactam biosynthetic genes for isopenicillin N epimerase and deacetoxycephalosporin C acetyltransferase
 A;Reference number: Z26033; MUID:90299822; PMID:1694525
 A;Accession: T52311
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-398 <KCV>
 A;Cross-references: EMBL:M32324; PIDN:AAA26714.1
 C;Genetics:
 A;Gene: cefD

Query Match 30.9%; Score 54; DB 2; Length 398;
 Best Local Similarity 53.3%; Pred. No. 9.8;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 831 IFLSRHCPINVGYGGGLKWL 851

Query Match 33.1%; Score 58; DB 2; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 6.8;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VSLSYRPCRFFGGGLKWIQ 23
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
 C;Accession: T35594
 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21583
 A;Accession: T35594
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-233 <SAU>
 A;Cross-references: EMBL:AL031317; PIDN:CAA20421.1; GSPDB:GN00070; SCOEDB:SCG64.43C
 A;Experimental source: strain A3(2)
 A;Genetics:
 A;Gene: SCOEDB:SCG64.43C
 C;Superfamily: hypothetical protein HI0278

Query Match 32.0%; Score 56; DB 2; Length 233;
 Best Local Similarity 44.0%; Pred. No. 3.2;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 SYRPCRFFGG--GGLKWIQEYLEK 28
 C;Species: Streptomyces clavuligerus
 C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-200

RESULT 12

C64104 gamma-aminobutyrate aminotransferase (EC 2.6.1.-) - *Haemophilus influenzae* (strain Rd K9C;Species: *Haemophilus influenzae*

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C;Accession: C64104; JCS879

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehn, C.L.; McDonald, I.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: C64104

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-454 <FIGR>

A;Cross-references: GB:U32776; GB:L42023; NID:91573969; PIDN:AAC22610.1; PID:91573974; T

R;Ikai, H.; Yamamoto, S. Biol. Pharm. Bull. 21, 170-173, 1998

A;Title: Two genes involved in the 1,3-diaminopropane production pathway in *Haemophilus*

A;Reference number: JC5879; MUID:98173550; PMID:9514614

A;Accession: JC5879

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-454 <IKA>

A;Cross-references: GB:U32776; NID:91573969; PIDN:AAC22610.1; PID:91573974

C;Comment: This enzyme is involved in the pathway of 1,3-diaminopropane synthesis.

C;Genetics:

A;Note: neither the complete nucleic acid sequence nor the complete translation are show

C;Superfamily: beta-alanine-pyruvate transaminase

C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate (Lys) (covalent) #status predicted

F;287/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 30.3%; Score 53; DB 2; Length 454;

Best Local Similarity 38.5%; Pred. No. 15; Mismatches 10; Indels 3; Gaps 0;

Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFGGGLKWIQEYLE 27

Db 181 PYPHEYRCPCPFGGAGAKAVEQYFE 206

RESULT 13

T46814 gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhba [imported] - *Rhizobium meliloti*C;Species: *Rhizobium meliloti*

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000

C;Accession: T46814

R;Lynch, D.; O'Connell, M.; O'Brien, J.

Submitted to the EMBL Data Library, December 1998

A;Description: Cloning and sequence analysis of the *Sinorhizobium meliloti* 2011 rhizobad

A;Reference number: Z24097

A;Accession: T46814

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-470 <LYN>

A;Cross-references: EMBL:AF110737; PIDN:AAD09412.1

A;Experimental source: strain 2011

C;Genetics:

A;Gene: rhba

C;Function:

A;Pathway: siderophore biosynthesis

C;Superfamily: beta-alanine-pyruvate transferase

C;Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16; Mismatches 10; Indels 6; Gaps 2;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPCRFGGG--LKWIQEYLEKAL 30

Db 198 PYPYAYRCP--FGGGNETATLAAEYFERAL 226

RESULT 14

B95419 gamma-aminobutyrate-pyruvate transaminase (EC 2.6.1.46) Rhba [imported] - *Sinorhizobium m*C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 02-Aug-2002

C;Accession: B95419

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler, F.; B

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meli*

A;Reference number: A95262; MUID:21368234; PMID:11474104

A;Accession: B95419

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-470 <KUR>

A;Cross-references: GB:AE006469; PIDN:AAK65916.1; PID:914524429; GSPDB:GN00165

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubl

peila, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R

L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001

A;Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau

hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: rhba

A;Genome: plasmid

C;Superfamily: beta-alanine-pyruvate transaminase

C;Keywords: aminotransferase

Query Match 30.3%; Score 53; DB 2; Length 470;

Best Local Similarity 43.8%; Pred. No. 16; Mismatches 14; Indels 2; Gaps 2;

Matches 14; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 2 PVSLSYRCPCRFGGG--LKWIQEYLEKAL 30

Db 198 PYPYAYRCP--FGGGNETATLAAEYFERAL 226

RESULT 15

T46814 AI3489 cytochrome c-552 [imported] - *Brucella melitensis* (strain 16M)C;Species: *Brucella melitensis*

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 02-Apr-2002

C;Accession: AI3489

R;Del Vecchio, V.G.; Kaprari, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov

; Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.; Let

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melit*

A;Reference number: AD3252; PMID:11756688

A;Accession: AI3489

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-202 <KUR>

A;Cross-references: GB:AE008917; PIDN:AA153084.1; PID:917983947; GSPDB:GN00190

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BME1903

A;Map position: 1 C;Superfamily: membrane-bound cytochrome cycM; cytochrome c homology

C;Keywords: chromoprotein; heme; iron; metalloprotein

F;84, 87/Binding site: heme (Cys) (covalent) #status predicted

F;88/Binding site: heme iron (His) (axial ligand) #status predicted

F;153/Binding site: heme iron (Met) (axial ligand) #status predicted

Query Match 28.6%; Score 50; DB 2; Length 202;

Best Local Similarity 44.0%; Pred. No. 19; Mismatches 11; Indels 12; Gaps 0;

Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 PVSLSYRCPCRFGGG--LKWIQEYLEKAL 30

Thu Oct 9 16:39:00 2003

us-09-835-107a-11.rpr

Page 5

Qy 6 SYRPCPCREFGGGLKWIQEYLEKAL 30
| | ; | | | : | |
117 SYSAAMKERAAGNWKDFEHLNKFL 141

Search completed: October 9, 2003, 09:21:32
Job time : 42 secs

OM protein - protein search, using sw model
Run on: October 9, 2003, 09:17:41 ; Search time 22 seconds
(without alignments)
66.265 Million cell updates/sec

Title: US-09-835-107A-11
perfect score:
175
Sequence: 1 KPVSLSYRCPCREFGGGLKWIQEYLEKALN 31

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	117	66.9	89	1 SDF1_MOUSE
2	117	66.9	93	1 SDF1_FELCA
3	117	66.9	93	1 SDF1_HUMAN
4	30.9	397	1 CERF_STRL	
5	30.9	955	1 B3A4_RABBIT	
6	30.3	454	1 DAT_HAEIN	
7	30.3	470	1 RHEB_RHIME	
8	30.3	529	1 PDP2_HUMAN	
9	29.7	983	1 B3A4_HUMAN	
10	29.1	282	1 HXCC_HUMAN	
11	28.6	530	1 PDP2_RAT	
12	28.0	508	1 GLPK_MYCLE	
13	28.0	517	1 GLPK_MYCTU	
14	28.0	557	1 TR2M_PSESS	
15	28.0	1714	1 YP93_CAEEL	
16	27.7	257	1 PERB_PROMA	
17	27.4	331	1 FCE2_MOUSE	
18	27.4	593	1 VG13_BPML5	
19	27.4	661	1 PDAT_YEAST	
20	27.4	1429	1 LIL2_MOUSE	
21	27.1	430	1 TCO2_MOUSE	
22	26.9	203	1 SN2B_CARAU	
23	26.9	398	1 CEFD_NOCLA	
24	26.9	409	1 TGF3_PIG	
25	26.9	507	1 GLK2_STRCO	
26	26.9	623	1 PDAT_SCHPO	
27	26.3	212	1 Y010_MYCPN	
28	26.3	390	1 ACKA_MYCPN	
29	26.0	387	1 KRL6_HSV1	
30	25.7	351	1 KAPL_APPLCA	
31	25.7	373	1 DNAJ_CAMJE	
32	25.7	393	1 ACKA_MIGGE	
33	25.7	577	1 YQ4B_CAEEL	

ALIGNMENTS

34 45 25.7 89 1 SYA_AQUPY
35 45 25.7 1142 1 JAK1_HUMAN
36 45 25.7 1153 1 JAK1_MOUSE
37 44.5 25.4 198 1 MYTR_MITCE
38 44.5 25.4 288 1 FPG_RALSO
39 44.5 25.4 501 1 TRA2_HUMAN
40 44.5 25.4 511 1 FAST_MOUSE
41 44 25.1 322 1 Y493_AQUAE
42 44 25.1 373 1 GLNA_MOUSE
43 44 25.1 409 1 RFL1_METKA
44 44 25.1 499 1 GLPK_XYLFA
45 44 25.1 562 1 TR2M_PANAY

09xdm3 aquifex pyr
P23458 homo sapien
P52332 mus musculus
P39047 mitrocoma c
O8y2d7 ralstonia s
Q12933 homo sapien
Q9jix9 mus musculus
O66783 aquifex aero
P15105 mus musculus
Q8txb5 methanopyrus
Q9pb76 xylella fastidiosa
Q47861 pantoea agg

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GenCore version 5.1.6
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Run on: October 9, 2003, 09:17:41 ; Search time 22 seconds
(without alignments)
66.265 Million cell updates/sec

RESULT 1

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DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating factor) (TLSF).			
DE	DE			
DE	CXCL12 OR SDFL1.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX				
RN				
RP				
RX				
RA	Nagasaki T., Kikutani H., Kishimoto T.; "Molecular cloning and structure of a pre-B-cell growth-stimulating factor"; RT			
RT	"Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.";			
RT	Science 261:600-603(1993).			
RN				
RP				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=94181581; PubMed=8134392; Nagasaki T., Kikutani H., Kishimoto T.; "Molecular cloning and structure of a pre-B-cell growth-stimulating factor"; RT			
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RA	MEDLINE=93342488; PubMed=83442023; Tashiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.; "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins.";			
RT	Weinstein I.B.; RT			
RT	"Molecular cloning of TPARI, a gene whose expression is repressed by the tumor Promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."; RT			
RT	EXP. Cell Res. 215:284-293(1994).			
RX				
RX	MEDLINE=95073497; PubMed=7982471; Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinsten I.B.; RT			
RA	"Molecular cloning of TPARI, a gene whose expression is repressed by the tumor Promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."; RT			
RT	EXP. Cell Res. 215:284-293(1994).			
RX				
RX	SEQUENCE FROM N.A.			
RX	MEDLINE=95073497; PubMed=7982471; Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.; RT			
RA	"Molecular cloning of TPARI, a gene whose expression is repressed by the tumor Promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."; RT			
RA	Submittion (DEC-1994) to the EMBL/GenBank/DDBJ databases.			
RL	-I- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, BUT NOT NEUTROPHILS.			
CC	-I- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE STROMAL CELL-DEPENDENT B-CELL CLONE DW34 CELLS.			
CC	-I- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=Alpha; IsoId=P40224-1; Sequence=Displayed;			
CC	Name=Beta; IsoId=P40224-2; Sequence=VSP_001057;			
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).			
CC	Q17426 caenorhabditis			

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Liver;
 RA Begum N.A.; Barnard G.F.;
 RT "Nucleotide sequence of hIRH, human intercrine reduced in
 hepatomas.", Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RT STRUCTURE BY NMR OF 22-88.
 RX MEDLINE=98046030; PubMed=9384579;
 RA Crump M.P., Gong J.H., Loetscher P., Rajarathnam K., Amara A.,
 Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
 Clark-Lewis I.;
 RT "Solution structure and basis for functional activity of stromal
 cell-derived factor-1; dissociation of CXCR4 activation from binding
 and inhibition of HIV-1.";
 RL EMBO J. 16:6996-7007(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
 RX MEDLINE=98284037; PubMed=9618518;
 RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
 RA Lolli E.;
 RT "Crystal structure of chemically synthesized [N33A] stromal
 cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
 coreceptor.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
 CC -!- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
 NOT NEUTROPHILS.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Beta;
 CC IsoId=P48061-1; Sequence=Displayed;
 CC
 CC ISOID=P48061-2; Sequence=VSP_001056;
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXC).
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U16752; AAA97434.1; -.
 DR EMBL; L36033; AAB39332.1; -.
 DR EMBL; L36034; AAB39333.1; -.
 DR EMBL; U19495; AAB40516.1; -.
 DR PIR; G01540; G01540.
 DR PDB; 1SDF; 28-JAN-98.
 DR PDB; 2SDF; 17-JUN-98.
 DR PDB; 1A15; 12-AUG-98.
 DR PDB; 1QG7; 28-FEB-01.
 DR Genew; HGNC:10672; CXCL12.
 DR MTM; 600835; -.
 DR GO; GO:003800; F:antiviral response protein activity; TAS.
 DR GO; GO:008009; F:chemokine activity; TAS.
 DR GO; GO:006874; P:calcium ion homeostasis; TAS.
 DR GO; GO:007155; P:cell adhesion; TAS.
 DR GO; GO:006935; P:chemotaxis; TAS.
 DR GO; GO:008015; P:circulation; TAS.
 DR GO; GO:007186; P:G-protein coupled receptor protein signaling; TAS.
 DR GO; GO:006955; P:immune response; TAS.
 DR GO; GO:008064; P:regulation of actin polymerization and/or d...; TAS.
 DR GO; GO:0009615; P:response to viruses; TAS.
 DR GO; GO:007165; P:signal transduction; TAS.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
 KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
 KW 3D-structure.

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
 FT DISULFID 30 55
 FT DISULFID 32 71 Missing (in isoform Alpha).
 FT VARSPLC 90 93 /FTId=VSP_001056.
 FT STRAND 36 36
 FT STRAND 41 43 HELIX
 FT TURN 53 55
 FT STRAND 56 63
 FT TURN 64 66
 FT STRAND 69 72
 FT TURN 74 75
 FT HELIX 77 85
 FT TURN 86 87
 FT SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query	Match	Score	DB	Length
QY	1 KPVSLSYRCPCRCFFGG-----GGLKWIQE 24	22	KPVSLSYRCPCRCFFESHHVARANVKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIE 81	
Dy	25 YLEKALN 31	82	YLEKALN 88	
Db				

RESULT 4
 CEFID_STRCL ID CEFID_STRCL STANDARD; PRT; 397 AA.
 AC P18549;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Isopenicillin N epimerase (EC 5.1.1.17).
 GN CEFID.
 OS Streptomyces clavuligerus.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1901;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ATCC 27064 / DSM 738 / NRRL 3585;
 RX MEDLINE=90299822; PubMed=1694525;
 RA Kovacevic S., Tobin M.B., Miller J.R.;
 RT "The beta-lactam biosynthesis genes for isopenicillin N epimerase and
 deacetoxypehalosporin C synthetase are expressed from a single
 transcript in Streptomyces clavuligerus.";
 RT J. Bacteriol. 172:3952-3958(1990).
 RN [2]
 RP SEQUENCE OF 1-23.
 RX MEDLINE=90028393; PubMed=2804141;
 RA Usui S., Yu C.-A.;
 RT "Purification and Properties of isopenicillin N epimerase from
 Streptomyces clavuligerus";
 RT Biochim. Biophys. Acta 999:78-85(1989);
 CC -!- FUNCTION: Catalyzes the reversible isomerization between
 isopenicillin N and penicillin N.
 CC -!- CATALYTIC ACTIVITY: Isopenicillin N = penicillin N.
 CC -!- COFACTOR: Pyridoxal phosphate.
 CC -!- PATHWAY: Cephalosporin antibiotics biosynthesis.
 CC -!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
 aminotransferases.
 CC
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RT "two genes involved in the 1,3-diaminopropane production pathway in
 RT *Haemophilus influenzae*";
 RL Biol. Pharm. Bull. 21:170-173(1998).
 CC -!- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-
 CC glutamate + L-aspartic 4-semialdehyde.
 CC -!- COFACTOR: Pyridoxal phosphate (Potential).
 CC -!- PATHWAY: 1,3-diaminopropane biosynthesis.
 CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
 aminotransferases.
 CC
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 CC
 CC EMBL; U32776; AAC22610.1; -.
 DR PIR; J64104; C64104.
 DR HSSP; P12995; 1QJ3.
 DR TIGR; H10949; -.
 DR InterPro; IPR005814; Aminotrans_3.
 DR InterPro; IPR004637; Dat.
 DR Pfam; PF00202; aminotran_3; 1.
 DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
 KW TRANSFERASE; Aminotransferase; Pyridoxal phosphate (POTENTIAL).
 FT BINDING 287 287 PYRIDOXAL PHOSPHATE (POTENTIAL).
 SQ SEQUENCE 454 AA; 49368 MW; B4B26F3AB7C55063 CRC64;

Query Match 30.3%; Score 53; DB 1; Length 454;
 Best Local Similarity 38.5%; Pred. No. 3.6; Mismatches 10; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 2 PVSLSYRPCRCRFGGGLKWIQEYLE 27
 Db 181 PYPHEYRCPPFGIGGEGAKAVEQYFE 206

RESULT 7

ID RHB_A_RHIME	STANDARD;	PRT;	470 AA.
AC 0923R2;			
DT 30-MAY-2000 (Rel. 3.9, Created)			
DT 30-MAY-2000 (Rel. 3.9, Last sequence update)			
DT 28-FEB-2003 (Rel. 4.1, Last annotation update)			
DE Diaminobutyrate--2-oxoglutarate aminotransferase (EC 2.6.1.76) (L- DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase) (DABA- DE aminotransferase) (DABA-AT) (L-2,4-diaminobutyrate:2-ketoglutarate 4- DE aminotransferase).			
DE RhizBA OR RhsA OR Ral1258 OR SMA2400.			
GN OS Rhizobium meliloti (<i>Sinorhizobium meliloti</i>). OG Plasmid pSymA (megaplasmid 1).			
OC Bacteria; Proteobacteria; Alphaproteobacteria; OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.			
OX NCBI_TAXID=382;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=RCR2011 / SU47;			
RX MEDLINE=21172875; PubMed=11274118;			
RA Lynch D.; O'Connell M.; Clarke P., Cuiv P.O., Crosa J.H.,			
RA "Genetic organization of the region encoding regulation, biosynthesis, and transport of rhizobactin 1021, a siderophore produced by Sinorhizobium meliloti"; RL J. Bacteriol. 183:2576-2585(2001). RN [2]			
RP SEQUENCE FROM N.A.			
RC STRAIN=1021;			
RX Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P., RA Barlow-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,			

RESULT 8

ID PDP2_HUMAN	STANDARD;	PRT;	529 AA.
AC Q9P2J9;			
DT 16-OCT-2001 (Rel. 4.0, Created)			
DT 16-OCT-2001 (Rel. 4.0, Last sequence update)			
DT 15-SEP-2003 (Rel. 4.2, Last annotation update)			
DE [Pyruvate dehydrogenase (Lipoamide)]-Phosphatase 2, mitochondrial DE precursor (EC 3.1.3.43) (PDP2) (Pyruvate dehydrogenase phosphatase, DE catalytic subunit 2) (PDPC 2).			
GN PDP2 OR KIAA1348.			
OS Homo sapiens (Human).			
OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX NCBI_TAXID=9605;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RX MEDLINE=20181126; PubMed=10718198;			
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.,			
RT "Prediction of the coding sequences of unidentified human genes. XVI. RT The complete sequences of 150 new cDNA clones from brain which code RT for large proteins in vitro.";			
RL DNA Res. 7:65-73(2000).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain;			
RX MEDLINE=22388257; PubMed=12477932;			

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Genomic and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
 REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
 PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] phosphate
 + H(2)O = [Pyruvate dehydrogenase (lipoamide)] + Phosphate.
 CC -!- COFACTOR: MAGNESIUM DEPENDENT (BY SIMILARITY).
 CC -!- SUBUNIT: HETERO-DIMER OF A CATALYTIC SUBUNIT AND A FAD PROTEIN OF
 UNKNOWN FUNCTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (BY similarity).
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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 CC -!- TISSUE SPECIFICITY: BELONGS TO THE PP2C FAMILY.
 CC DR EMBL; AB037769; BAA92586.1; ALT_INIT.
 CC DR EMBL; BC028030; AAH28030.1; -.
 CC DR SMART; SM00332; PP2Cc; 1.
 CC DR InterPro; IPR001932; PP2C-like.
 CC DR InterPro; IPR000222; PP2C.
 CC DR Pfam; PF00481; PPC2; 2.
 CC DR SMART; SM00331; PP2C_SIG; 1.
 CC DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Mitochondrion; transit peptide; Magnesium.
 FT TRANSIT 1 66 529 MITOCHONDRIUM (POTENTIAL)
 FT CHAIN 67 529 [PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-
 FT PHOSPHATASE 2
 SQ SEQUENCE 529 AA; 59978 MW; 252CAEBCDAF61A5C CRC64;
 Query Match 30.3%; Score 53; DB 1; Length 529;
 Best Local Similarity 46.2%; Pred. No. 4.2; Mismatches 8; Indels 4; Gaps 1;
 Matches 12; Conservative 2; Mismatches 1;
 QY 10 PCRFEGGGGKWKIQE---YLEKALN 31
 ||| ||| ||| :||| !|:
 DB 344 PCRAFGDVQLKWSKELQRSILERGFN 369
 RESULT 9
 B3A4_HUMAN
 ID B3A4_HUMAN STANDARD PRT; 983 AA.
 AC Q96Q91; Q96RM5; Q9BXF2; Q9BXN3;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Anion exchange protein 4 (Anion exchanger 4) (Sodium bicarbonate
 DE cotransporter 5).
 GN SLC4A9 OR AE4 OR SBC5.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 OC RXN [1]
 OC RP SEQUENCE FROM N.A. (ISOFORM 2).
 OC RC TISSUE=Kidney, and Testis;
 OC RX MEDLINE=2119380; PubMed=11302728;
 OC RA Parker M.D., Ourmozdi E.P., Tanner M.J.A.;
 OC RT "Human BTR1, a new bicarbonate transporter superfamily member and
 OC RT human AE4 from kidney.";
 OC RL Biochem. Biophys. Res. Commun. 282:1103-1109(2001).
 OC RN [2]
 OC RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 OC RC TISSUE=Kidney;
 OC RL duplicated region: SLC4A9 at 5q31.;"
 OC RN Genome Biol. 2:RESEARCH0011.1-RESEARCH0011.13(2001).
 OC RN [3]
 OC RP Lipovich L., Lynch E.D., Lee M.K., King M.-C.;
 OC RT "A novel sodium bicarbonate cotransporter-like gene in an ancient
 OC RP duplicated region: SLC4A9 at 5q31.";
 OC RL Genome Biol. 2:RESEARCH0011.1-RESEARCH0011.13(2001).
 OC RN SEQUENCE FROM N.A. (ISOFORM 3).
 OC RA Karet F.E.;
 OC RT "Cloning and characterization of human AE4.";
 OC RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 OC RN [4]
 OC RP SEQUENCE OF 3-983 FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY.
 OC RC TISSUE=Testis;
 OC RA Ishibashi K.;
 OC RT "Molecular cloning of human sodium bicarbonate cotransporter 5.";
 OC RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 OC CC -!- FUNCTION: Probable apical anion exchanger of the kidney cortex (By
 OC CC similarity).
 OC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 OC CC -!- ALTERNATIVE PRODUCTS:
 OC CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC Name=2;
 CC IsoID=Q96Q91-1; Sequence=Displayed;
 CC CC Name=3;
 CC CC IsoID=Q96Q91-3; Sequence=VSP_007085, VSP_007086, VSP_007087;
 CC CC -!- TISSUE SPECIFICITY: Kidney-specific.
 CC CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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 CC -!- TISSUE SPECIFICITY: BELONGS TO THE ANION EXCHANGER FAMILY.
 CC DR EMBL; AF336237; AAK16733.1; -.
 CC DR EMBL; AF313465; AAK28832.1; ALT_INIT.
 CC DR EMBL; AB032762; BAA93010.1; -.
 CC DR HSSP; P02730; IBWX.
 CC DR Genew; HGNC:11035; SLC4A9.
 CC DR InterPro; IPR001717; Anion-exchange.
 CC DR InterPro; IPR003020; HCO3_cotransp.
 CC DR Pfam; PF00955; HCO3_cotransp; 1.
 CC DR PRINTS; PR01231; HCO3TRANSPORT.
 CC DR TIGRFAMs; TIGR00834; ae; 1.
 CC KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
 CC KW Anion exchange; Alternative splicing.
 CC DOMAIN 1 414 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 415 983 MEMBRANE (ANION EXCHANGE).
 CC FT TRANSMEM 415 435 POTENTIAL.
 CC FT TRANSMEM 443 463 POTENTIAL.
 CC FT TRANSMEM 465 485 POTENTIAL.
 CC FT TRANSMEM 500 520 POTENTIAL.
 CC FT TRANSMEM 530 550 POTENTIAL.
 CC DOMAIN 552 623 EXOPLASMIC LOOP (POTENTIAL).

Query Match Score 29.7%; DB 1; Length 983;
 Best Local Similarity 44.0%; Pred. No. 11;
 Matches 11; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 1 KPVSLSYRCPCRCFFGGG - LKWIQ 23
 Db 558 KPGSSAYGCLCQYPPGGGNESQWIR 582

RESULT 10

ID HXCC_HUMAN	STANDARD;	PRT;	282 AA.
AC P31275;	Q9BXJ6;		
DT 01-JUL-1993 (Rel. 26, Created)			
DT 28-FEB-2003 (Rel. 41, Last sequence update)			
DE Homeobox protein Hox-C12 (Hox-3F).			
GN HOXC12 OR HOX3F.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA "A complete mutation analysis Panel of human HOX genes.";			
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE OF 214-279 FROM N.A.			
RX MEDLINE=90098876; PubMed=2574852;			
RA Accampora D., D'Esposito M., Faella A., Pannese M., Migliaccio E., Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;			
RT "The human HOX gene family.";			
RL Nucleic Acids Res. 17:10385-10402(1989).			
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.			
CC -!- SUBCELLULAR LOCATION: Nuclear.			
CC -!- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.			
CC			
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CC			
CC EMBL; AF328962; AAK16717.1; JOINED.			
DR PIR; S14933; S14933.			
DR HSSP; P14653; 1B72.			
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE	282 AA;	30171 MW;	493C53C511054A4D CRC64;
DR TRANSFAC; T03329; -.			
DR Genew; HGNC; 5124; HOXC12.			
DR MIM; 142975; -.			
DR InterPro; IPR01356; Homeobox.			
DR Pfam; PF00046; homeobox; 1.			
DR PRINTS; PR00024; HOMEobox.			
DR ProDom; PD00010; Homeobox; 1.			
DR SMART; SM00389; HOX; 1.			
DR PROSITE; PS50071; HOMEobox_2; 1.			
KW Homeobox; DNA-binding; Developmental Protein; Nuclear protein; Transcription regulation.			
FT DNA_BIND	2124	273	HOMEobox.
FT SEQUENCE			

Thu Oct 9 16:39:01 2003

DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Mitochondrion; Transit peptide; Magnesium.
 FT TRANSIT 1 67 MITOCHONDRION (POTENTIAL);
 CHAIN 68 530 [PYRUVATE DEHYDROGENASE [LIPOAMIDE]] -
 FT
 SQ SEQUENCE 530 AA; 59654 MW; 5AB688FACT78AD9CD CRC64;
 PHOSPHATASE 2.
 Query Match 28.6%; Score 50; DB 1; Length 530;
 Best Local Similarity 47.6%; Pred. No. 12; Mismatches 6; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
 Qy 10 PCRFEGGGGLKWIQEYLEKAL 30
 DB 345 PCRAFGDVQWKWSKELQRNVL 365

RESULT 12
 GLPK_MYCLE STANDARD; PRT; 508 AA.

ID GLPK_MYCLE
 AC 09CB81;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 DE (Glycerokinase) (GK).
 GN GLPK OR ML2314.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC
 OC
 OX NCBI_TaxID=1769;
 RN RX STRAIN=TN;
 RP RC SEQUENCE FROM N.A.
 MEDLINE=21128732; PubMed=11234002;
 Cole S.T., Eiglemeier K., Parkhill J., James K.D., Thomson N.R.,
 Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -!- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND
 CC METABOLISM.
 CC -!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
 CC -!- PATHWAY: Glycerol utilization; rate-limiting step.
 CC -!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
 CC GLYCEROKINASE / XYLULOKINASE FAMILY.
 CC
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 CC
 CC EMBL; ALI583925; CAC31830.1; -.
 DR PIR; F87198; F87198.
 DR HSSP; P08859; IGLC.
 DR Leproma; ML2314; -
 DR HAMAP; MF_00186; -; 1.
 DR InterPro; IPR00577; FGGY_kin.
 DR InterPro; IPR00599; Glycerol_kin.
 DR Pfam; PF00370; FGGY; 1.
 DR Pfam; PF02782; FGGY_C; 1.
 DR TIGRFAMS; TIGR01311; glycerol_kin; 1.
 DR PROSITE; PS00933; FGGY_KINASES_1; 1.
 DR PROSITE; PS00445; FGGY_KINASES_2; 1.
 KW Glycerol metabolism; Transferase; Kinase; ATP-binding;

KW Complete proteome.
 FT NP_BIND 156 ATP (PROBABLE);
 SQ SEQUENCE 508 AA; 54658 MW; A15379793ECFF4039 CRC64;
 Query Match 28.0%; Score 49; DB 1; Length 508;
 Best Local Similarity 44.4%; Pred. No. 16; Mismatches 4; Indels 6; Gaps 0;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 10 PCRFEGGGGLKWIQEYLE 27
 Db 134 PATYFSGGKLQWILEND 151

RESULT 13
 GLPK_MYCTU STANDARD; PRT; 517 AA.

ID GLPK_MYCTU
 AC 069554;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
 DE (Glycerokinase) (GK).
 GN GLPK OR RV3696C OR MT3798 OR MTV025.044C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN RX STRAIN=H37Rv;
 RP RC SEQUENCE FROM N.A.
 MEDLINE=98295987; PubMed=9634230;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP RC SEQUENCE FROM N.A.
 MEDLINE=98295987; PubMed=9634230;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP RC SEQUENCE FROM N.A.
 MEDLINE=98295987; PubMed=9634230;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP RC SEQUENCE FROM N.A.
 MEDLINE=98295987; PubMed=9634230;
 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglemeier K., Gas S., Barry C.E. III, Tekala F.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AL022121; CAA18018.1; -.
 DR EMBL; AE007177; AAK48165.1; -.
 DR PIR; A70793; A70793.
 DR HSSP; P08859; IGLC.
 DR TIGR; MT3798; -.

Query Match 28.0%; Score 49; DB 1; Length 557;
 Best Local Similarity 43.5%; Pred. No. 17;
 Matches 10; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 9 CPCRFFGGGLKWIQEYLEKALN 31
 | | | | | | | | | | | | | | | | | | | |
 Db 511 CSCSFAGG---WIECAVQTAQN 529

DR Tuberculist; Rv3696c; -.
 DR HAMAP; MF_00186; -; 1.
 DR InterPro; IPR000577; FGGY_kin.
 DR InterPro; IPR005999; Glycerol_kin.
 DR Pfam; PF00370; FGGY; 1.
 DR Pfam; PF02782; FGGY_C; 1.
 DR TIGRFAMS; TIGR01311; glycerol_kin; 1.
 DR PROSITE; PS00445; FGGY_KINASES_2; 1.
 DR PROSITE; PS00933; FGGY_KINASES_1; 1.
 KW Glycerol metabolism; Transferase; Kinase; ATP-binding;
 KW NP_BIND; Complete proteome.
 FT SEQUENCE 517 AA; 55859 MW; 7E3F30DCF2A1E63E CRC64;

Query Match 28.0%; Score 49; DB 1; Length 517;
 Best Local Similarity 44.4%; Pred. No. 16;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 10 PCREFGGGLKWIQEYLE 27
 | : | | | | | | | | | | | | | | | | | | | |
 Db 143 PATYFSGGKLQWILENVD 160

RESULT 14
 TR2M_PSESS
 ID TR2M_PSESS
 AC P06617;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Tryptophan 2-monoxygenase (EC 1.13.12.3).
 GN IAA.
 OS Pseudomonas syringae (pv. savastanoi).
 OG Plasmid PIAA1.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC NCBI_TaxID=29438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EW2009;
 RA Yamada T., Palm C.J., Brooks B., Kosuge T.;
 RT "Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid genes show homology with Agrobacterium tumefaciens T-DNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6522-6526(1985).
 CC -!- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide + CO(2) + H(2)O.
 CC -!- PATHWAY: Biosynthesis of auxins from tryptophan; first step.
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 CC REVISIONS.
 RA Waterston R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SK12 SUBFAMILY.
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 CC EMBL; U20861; AAA62291.2;
 DR WormPep; C28H8.3; CE29195.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
 KW Nuclear protein.
 FT NP_BIND 607 614 ATP (POTENTIAL).
 FT NP_BIND 806 813 ATP (POTENTIAL).
 FT SITE 913 916 DEVH BOX.
 FT SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;

Query Match 28.0%; Score 49; DB 1; Length 1714;
 Best Local Similarity 48.1%; Pred. No. 51;
 Matches 13; Conservative 1; Mismatches 7; Indels 6; Gaps 2;

QY 10 PCREFGGGLK--WIQ---EYLEKAL 30
 | | | | | | | | | | | | | | | | | | | |
 Db 1058 PCKFFGQHGTAKAVWISSELRLLENAL 1084

Search completed: October 9, 2003, 09:18:15
 Job time : 25 secs

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OM protein - protein search, using sw model

Run on:	October 9, 2003, 09:17:42 ; Search time 95 Seconds (without alignments)
	84.207 Million cell updates/sec
Title:	US-09-835-107A-11
Perfect score:	175 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Sequence:	
Scoring table:	BLOSUM62
Searched:	Gapop 10.0 , Gapext 0.5
total number of hits satisfying chosen parameters:	830525
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	
1:	SPTREMBL_23:*
2:	sp_archea:*
3:	sp_bacteria:*
4:	sp_fungi:*
5:	sp_human:*
6:	sp_invertebrate:*
7:	sp_mammal:*
8:	sp_mhc:*
9:	sp_organelle:*
10:	sp_phage:*
11:	sp_plant:*
12:	sp_rodont:*
13:	sp_vertebrate:*
14:	sp_unclassified:*
15:	sp_rvirus:*
16:	sp_bacteriap:*
17:	sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	117	66.9	89	Q8HYPO macaca mulatta
2	117	66.9	92	Q9h554 homo sapien
3	114	65.1	89	Q9QZD1 rattus norvegicus
4	105	60.0	94	Q8UJ9 xenopus laevis
5	61	34.9	507	Q93YP8 arabidopsis thaliana
6	61	34.9	1084	Q048947 arabidopsis thaliana
7	61	34.9	1088	Q9SJ22 arabidopsis thaliana
8	60.5	34.6	974	Q93155 gossypium hirsutum
9	60.5	34.6	974	Q8W1W0 gossypium hirsutum
10	58	33.1	346	Q8L778 arabidopsis thaliana
11	58	33.1	366	Q94JQ6 arabidopsis thaliana
12	58	33.1	469	Q91168 pseudomonas aeruginosa
13	58	33.1	1069	Q9FB9 arabidopsis thaliana
14	58	33.1	1081	Q65338 arabidopsis thaliana
15	58	33.1	1084	Q9FGF9 arabidopsis thaliana
57.5	32.9	939	Q943H3 oryza sativa	

ALIGNMENTS

RESULT 1	ID	Q8HYPO	PRELIMINARY;	PRT;	89 AA.
Q8HYPO; AC Q8HYPO; DT 01-MAR-2003 (TREMBLrel. 23, Created)					
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DE Chemokine CXCL12/SDF-1ALPHA.					
CS Macaca mulatta (Rhesus macaque).					
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.					
OC Cercopithecinae; Macaca.					
OC NCBI_TaxID=9544;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;					
RT "Comprehensive cloning and sequencing reveals evolutionary conservation among all groups of rhesus macaque chemokines."					
RT Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.					
DR EMBL; AF449283; AAN76086.1; -					
SEQUENCE 89 AA; 10105 MW; AD531633C6DC2B07 CRC64;					
SQ					

Query Match 66.9%; Score 117; DB 6; Length 89;
Best Local Similarity 40.3%; Pred. No. 1.5e-09;
Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

Qy	1	KPVSLSYRCPCRFGG-----	GGLKWIQE 24
Db	22	KPVSLSYRCPCRFESHHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81	
Qy	25	YLEKALN 31	
Db	82	YLEKALN 88	

RESULT 2
Q9H554 ID Q9H554 PRELIMINARY; PRT; 92 AA.
AC Q9H554;

Query Match 01-MAR-2001 (TREMBLrel. 16, Created) |-----| GKLKIQE 24
 Best Local Similarity 01-MAR-2001 (TREMBLrel. 16, Last sequence update) |||||
 Matches 01-JUN-2002 (TREMBLrel. 21, Last annotation update) ||||| 81

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; SDF1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606; [1]

RP SEQUENCE FROM N.A.

RA Bird C.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; ALL37026; CAC10202.1; -. DR HSSP; P48061; 1SDF; InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1. DR SMART; SM00199; SCY; 1.
 FT NON_TER 1. DR SMART; SM00199; SCY; 1.
 SQ SEQUENCE 92 AA; 10510 MW; AEFOC402B44E8D20 CRC64;

Query Match 66.9%; Score 117; DB 4; Length 92; QY 1 KPVSLSYRCPCRFQGG-----GGLKWIQE 24
 Best Local Similarity 40.3%; Pred. No. 1.6e-09; AC |||||
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1; DR 22 KPVSLSYRCPCRFQESHHVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIQE 81

QY 25 YLEKALN 31 DR BRAUN M., WUNDERLIN M., KNOESEL W., GIERSCHIK P., MOEPPS B.;
 Db 82 YLEKALN 88 RT "XENOPUS LAEVIS STROMAL-DERIVED FACTOR 1; CONSERVATION OF STRUCTURE
 AND FUNCTION DURING VERTEBRATE DEVELOPMENT."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ278857; CAC82196.1; -. DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR SIGNAL 1 21 KW Signal.
 FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
 FT SIGNAL 1 21 KW Signal.
 SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 60.0%; Score 105; DB 13; Length 94; QY 1 KPVSLSYRCPCRFQGG-----GLKWIQE 24
 Best Local Similarity 35.8%; Pred. No. 9.4e-08; AC |||||
 Matches 24; Conservative 1; Mismatches 6; Indels 36; Gaps 1; DR 22 KPVSLSYRCPCRFQESHHVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIQE 81

QY 25 YLEKALN 31 DR RATTUS NORVEGICUS (RAT).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116; RN {1}

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; RA OHTANI Y., OKADA M., KAWAGUCHI N., MINAMI M., SATOH M.;
 RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
 alpha);"; RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RL Pillarissetti K., GUPTA S.K.; RT "Identification and molecular cloning of a novel rat ortholog of the
 alpha chemokine, stromal cell derived factor-1 (SDF-1)." ;
 RT Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AF189724; AAF01065.1; DR EMBL; AF209976; AAG43506.1; DR HSSP; P48061; 1SDF; DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1. DR SMART; SM00199; SCY; 1.
 DR SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 65.1%; Score 114; DB 11; Length 89; QY 1 KPVSLSYRCPCRFQGG-----GKLKIQE 24
 Best Local Similarity 38.8%; Pred. No. 4.2e-09; AC |||||
 Matches 26; Conservative 1; Mismatches 4; Indels 36; Gaps 1; DR BRAUN M., KARLIN-NEUMANN G., SOUTHWICK A., LAM B., MIRANDA M., NGUYEN M., KARLIN-NEUMANN G., SOUTHWICK A., LAM B., MIRANDA M., PALM C.J., BOWSER L., JONES T., BANH J., CARNINCI P., CHEN H., CHEUK R., CHUNG M.K., HAYASHIZAKI Y., ISHIDA J., KAMIYA A., KAWAI J., KIM C., LIN J., LIU S.X., NARUSAKA M., PHAM P.K., SAKANO H., SAKURAI T., SATOU M., SEKI M., SHINN P., YAMADA K., SHINOZAKI K.,

us-09-835-107a-11.rspt

RA	Ecker J., Theologis A., Davis R.W.;
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[2]	
RN	SEQUENCE FROM N.A.
RA	Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA	Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA	Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA	Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA	Ecker J., Theologis A., Davis R.W.;
RL	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY059858; AAL24340.1; -.
DR	EMBL; AY093308; AAM13307.1; -.
DR	InterPro; IPR005150; Cellulose_synt; 1.
DR	Pfam; PF03552; Cellulose_synt; 1.
RN	SEQUENCE 507 AA; 56665 MW; D04313743E31DE61 CRC64;
Query Match	34.9%; Score 61; DB 10; Length 1084;
Best Local Similarity	43.5%; Pred. No. 3.7;
Matches	10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY	3 VSLSYRPCPCRFGGGLKWIQEY 25
Db	: : : ; : : ;
Db	833 IFLSRHCPPIWYGIGGGLKWLRF 855
RESULT 6	
ID	048947 PRELIMINARY; PRT; 1084 AA.
AC	048947; PRELIMINARY; PRT; 1084 AA.
DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Cellulose synthase catalytic subunit.
GN	R-A OR T22F8.250 OR AT4G39350.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV, Columbia;
RX	MEDLINE=98111412; PubMed=9445479;
RA	Arioli T., Peng L., Betzner A.S., Burn J., Wittke W., Herth W.,
RA	Camilleri C., Hoffte H., Plazinski J., Birch R., Cork A., Glover J.,
RA	Redmond J., Williamson R.E.;
RT	"Molecular analysis of cellulose biosynthesis in Arabidopsis.";
RL	Science 279:717-720(1998).
RN	[2] SEQUENCE FROM N.A.
RP	Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I.,
RA	Mewes H.W., Mayer K.F.X., Schueler C.;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN	[3] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	[4] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	[5] SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RN	Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
RA	Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OX NCBI_TaxID=3635;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
 RA Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
 RA Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
 RA Theologis A.; Davis R.W.;
 RT the catalytic subunit of cellulose synthase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:12637-12642(1996).
 DR EMBL; U58283; AAB37766.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR Pfam; PF03552; Cellulose_synt; 1.
 DR Sequence 974 AA; 109703 MW; 2656CA2D05D100A7 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
 Best Local Similarity 54.5%; Pred. No. 3.9;
 Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKWIQ 23
 Db 721 IFLSRHCPPLWYGFGGGRLKWLQ 742

RESULT 9

Q8WIWO PRELIMINARY; PRT; 974 AA.
 ID Q8WIWO
 AC Q8WIWO;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cellulose synthase A4.
 GN CES4.
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608363; PubMed=11743074;

RA Kim H.J., Triplett B.A.;
 RT "Cotton Fiber Growth in Plant and in Vitro. Model's for Plant Cell
 Elongation and Cell Wall Biogenesis.",
 RL Plant Physiol. 127:1361-1366(2001).
 DR EMBL; AF413210; AAL37718.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR Pfam; PF03552; Cellulose_synt; 1.
 SQ Sequence 974 AA; 109499 MW; F8AFB66ABA2B8071 CRC64;

Query Match 34.6%; Score 60.5; DB 10; Length 974;
 Best Local Similarity 54.5%; Pred. No. 3.9;
 Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VSLSYRCPCRF-FGGGLKWIQ 23
 Db 721 IFLSRHCPPLWYGFGGGRLKWLQ 742

RESULT 10

Q8L778 PRELIMINARY; PRT; 346 AA.
 ID Q8L778
 AC Q8L778;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 GN ARSG09870.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
 RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Pham P.K., Ouach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF375439; AAK53023.1; -
 DR EMBL; AY143937; AAN28896.1; -
 DR InterPro; IPR005150; Cellulose_synt.
 DR Pfam; PF03552; Cellulose_synt; 1.
 SQ Sequence 366 AA; 40788 MW; A287A60060D3EE2B CRC64;

Query Match 33.1%; Score 58; DB 10; Length 366;
 Best Local Similarity 47.6%; Pred. No. 3.2;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 VSLSYRCPCRF-FGGGLKWIQ 23
 : ||| : |||||: :

Db 116 IFLSRHCPPIWYGGGLKWLE 136
 DR InterPro; IPR00184; ZF_RING; 1.
 DR Pfam; PF03552; Cellulose_synt; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 SQ 1069 AA; 120861 MW; D03ED5C578DB3E7C CRC64;

RESULT 12
 ID Q9I168 PRELIMINARY; PRT; 469 AA.
 AC Q9I168;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Probable class III aminotransferase.
 GN PA2413.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goitry L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 RA Brody L.J., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RL opportunistic pathogen.";
 DR EMBL; AE004668; AAG05801.1; -.
 DR HSSP; P16932; 2DKB.
 DR InterPro; IPR005814; Aminotrans_3.
 DR Pfam; PF00202; aminotran_3; 1.
 DR TIGRFAMS; TIGR00709; dat; 1.
 DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
 KW Transferase; Aminotransferase; Complete proteome.
 SQ SEQUENCE 469 AA; 50215 MW; FAAB575E88A44EE8 CRC64;

Query Match 33.1%; Score 58; DB 16; Length 469;
 Best Local Similarity 43.3%; Pred. No. 4.2;
 Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PVLSYRCPCRFGGGLKWIEYLEKALN 31
 Db 199 PYPYDYRCPCFGLGGGEAGVKANLHYLENLN 228

RESULT 13
 ID Q9FIB9 PRELIMINARY; PRT; 1069 AA.
 AC Q9FIB9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 OS *Arabidopsis thaliana* (Mouse-ear cress);
 OC *Bukaryota*; *Viridiplantae*; *Embryophyta*; *Tracheophyta*;
 OC *Spermatophyta*; *Magnoliophyta*; *eudicotyledons*; *core eudicots*;
 OC *eurosids II*; *Brassicales*; *Brassicaceae*; *Arabidopsis*.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=9156233; PubMed=10048488;
 RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seventeen physically assigned PI and TAC clones.";
 RT DNA Res. 5:379-391(1998).
 RL EMBL; AB016893; BAB09408.1; -.
 DR InterPro; IPR005150; Cellulose_synt.

RESULT 14
 ID 065338 PRELIMINARY; PRT; 1081 AA.
 AC 065338;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Cellulose synthase (Fragment).
 RA *Arabidopsis thaliana* (Mouse-ear cress).
 RA *Eukaryota*; *Viridiplantae*; *Streptophyta*; *Embryophyta*; *Tracheophyta*;
 OC *Spermatophyta*; *Magnoliophyta*; *eudicotyledons*; *core eudicots*; *Rosidae*;
 OC *eurosids II*; *Brassicales*; *Brassicaceae*; *Arabidopsis*.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_Columbia;
 RA Wu L., Joshi C.P., Chiang V.L.;
 RT "AraxCellA, a new member of the cellulose synthase gene family from
 RL *Arabidopsis* (Accession No. AF062485) (PGR98-114).";
 DR Plant Physiol. 117:1125-1125(1998).
 EMBL; AF062485; AAC29067.1;
 DR InterPro; IPR005150; Cellulose_synt.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF03552; Cellulose_synt; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 1081 AA; 122446 MW; DC59A35A1713FD9F CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1081;
 Best Local Similarity 47.6%; Pred. No. 10;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VSLSYRCPCRFGGGLKWQ 23
 Db 831 IFLSRHCPPIWYGGGLKWLE 851

RESULT 15
 ID Q9FGF9 PRELIMINARY; PRT; 1084 AA.
 AC Q9FGF9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Cellulose synthase catalytic subunit.
 OS *Arabidopsis thaliana* (Mouse-ear cress);
 OC *Arabidopsis thaliana*; *Viridiplantae*; *Embryophyta*; *Tracheophyta*;
 OC *Spermatophyta*; *Magnoliophyta*; *eudicotyledons*; *core eudicots*; *Rosidae*.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. XI.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB025637; BAB10307.1; -.
DR InterPro; IPR005150; Cellulose_synt.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF03552; Cellulose_synt; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 1084 AA; 122501 MW; 1520439A5053608C CRC64;

Query Match 33.1%; Score 58; DB 10; Length 1084;
Best Local Similarity 47.5%; Pred. No. 10;
Matches 10; Conservative 4; Mismatches 7; Index 0; Gaps 0;

QY 3 VSLSYRCRPCRFGGGLKWIQ 23
 : ||| : |||||:
Db 834 IFLSRHCPIWYGYGGGLKWL 854

Search completed: October 9, 2003, 09:20:47
Job time : 100 secs

OM protein - protein search, using sw model

Run on: October 9, 2003, 09:17:46 ; Search time 29 seconds
 (without alignments)
 45.229 Million cell updates/sec

Title: US-09-835-107A-11
 Perfect score: 175
 Sequence: 1 KPVSLISYRCPCRFEGGGK-WIQEYLEKALN 31
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA: *
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep: *
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/PECTUS_COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	66.9	89	1	US-08-181-556-2
2	117	66.9	89	1	US-08-323-084A-1
3	117	66.9	89	1	US-08-674-008-1
4	117	66.9	93	1	US-08-323-084A-5
5	117	66.9	93	1	US-08-674-008-5
6	117	66.9	93	4	US-09-312-283C-421
7	117	66.9	166	4	US-09-646-028-5
8	117	66.9	177	4	US-09-646-028-54
9	117	66.9	326	3	US-08-808-720-3
10	117	66.9	328	3	US-08-808-720-1
11	117	66.9	339	4	US-09-646-028-55
12	61	34.9	1084	4	US-09-221-013A-8
13	60.5	34.6	974	3	US-08-960-048-6
14	60.5	34.6	974	4	US-09-838-586-6
15	58	33.1	535	4	US-09-252-991A-25662
16	50	28.6	588	3	US-08-481-190-16
17	50	28.6	588	5	PCT-US93-00869-16
18	50	28.6	685	3	US-08-960-048-7
19	50	28.6	685	4	US-09-838-586-7
20	49	28.3	504	4	US-09-252-991A-32272
21	49	28.0	416	1	US-08-117-731A-29
22	49	28.0	488	4	US-08-311-731A-61
23	48	27.4	78	3	US-09-188-930-158
24	48	27.4	78	3	US-09-188-930-285
25	48	27.4	78	4	US-09-312-283C-158
26	48	27.4	78	4	US-09-312-283C-285
27	48	27.4	125	3	US-08-722-126A-7

Sequence 7, Appli
 Sequence 4, Appli
 Sequence 6, Appli
 Sequence 2, Appli
 Sequence 30180, A
 Sequence 26204, A
 Sequence 6, Appli
 Patent No. 5168051
 Sequence 20340, A
 Sequence 1215, Ap
 Sequence 40, Appli
 Sequence 114, Appli
 Sequence 17, Appli

RESULT 1
 US-08-181-556-2
 Sequence 2, Application US/08181556
 PATENT NO. 5525486
 GENERAL INFORMATION:
 APPLICANT: HONJO, Tasuku
 APPLICANT: TASHIRO, Kei
 TITLE OF INVENTION: PROCESS FOR CONSTRUCTING cDNA LIBRARY, AND NOVEL POLYPEPTIDE AND DNA CODING, FOR THE SAME
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEVENS, MILLER & MOSHER
 STREET: 515 NO. 55254866th Washington Street (P.O. Box 1427)
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22313

ALIGNMENTS

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/181,556
 FILING DATE: 14-JAN-1994
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 5-22098
 FILING DATE: 14-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: POULOS III, James A.
 REGISTRATION NUMBER: 31714
 REFERENCE/DOCKET NUMBER: TPP/29088
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 549-7200
 TELEFAX: (703) 528-5313
 TELEX: 89-2746

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 89 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-181-556-2

Query Match Score 117; DB 1; Length 89;
 Best Local Similarity 40.3%; Pred. No. 6.6e-09;
 Matches 0; Mismatches 4; Indels 36; Gaps 1;

Sequence 7, Appli
 Sequence 4, Appli
 Sequence 6, Appli
 Sequence 2, Appli
 Sequence 30180, A
 Sequence 26204, A
 Sequence 6, Appli
 Patent No. 5168051
 Sequence 20340, A
 Sequence 1215, Ap
 Sequence 40, Appli
 Sequence 114, Appli
 Sequence 17, Appli
 Sequence 17, Appli
 Sequence 17, Appli
 Sequence 17, Appli

NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037-3202

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,008
 FILING DATE: 1-JUL-1996
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 280505/1993
 FILING DATE: 14-OCT-1993

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7050
 TELEFAX: (202)293-7860
 TELEX: 6491103

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 89 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-674-008-1

Query Match 66.9%; Score 117; DB 1; Length 89;
 Best Local Similarity 40.3%; Pred. No. 6.6e-09; Pred. No. 6.6e-09;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

RESULT 4
 US-08-323-084A-5
 Sequence 5, Application US/08323084A
 ; Sequence 1, Application US/08674008
 ; Patent No. 5756084
 ; GENERAL INFORMATION:
 ; APPLICANT: HONJO, Tasuku
 ; APPLICANT: SHIROZU, Michio
 ; APPLICANT: TADA, Hideaki
 ; TITLE OF INVENTION: HUMAN STROMAL DERIVED FACTOR 1 AND 1 (AS Amended)
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20037-3202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/323, 084A
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 280505/1993
 FILING DATE: 14-OCT-1993
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060
 TELEX: 6491103
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 93 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-323-084A-5

Query Match 66.9%; Score 117; DB 1; Length 93;
 Best Local Similarity 40.3%; Pred. No. 6.9e-09; 0; Mismatches 4; Indels 36; Gaps 1;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
 Db 22 KPVSLSYRCPCRFFESVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIQE 81

QY 25 YLEKALN 31
 Db 82 YLEKALN 88

RESULT 5
 Sequence 5, Application US/08674008
 Patent No. 5756084
 GENERAL INFORMATION:
 APPLICANT: HONJO, Tasuku
 APPLICANT: SHIROZU, Michio
 APPLICANT: TADA, Hideaki
 TITLE OF INVENTION: HUMAN STROMAL DERIVED
 TITLE OF INVENTION: FACTOR 1 AND 1 (AS Amended)
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MCNAMARA & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20037-3202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674, 008
 FILING DATE: 1-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/323, 084
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 280505/1993
 FILING DATE: 14-OCT-1993
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)293-7060
 TELEX: 6491103
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 93 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-674-008-5

Query Match 66.9%; Score 117; DB 1; Length 93;
 Best Local Similarity 40.3%; Pred. No. 6.9e-09; 0; Mismatches 4; Indels 36; Gaps 1;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
 Db 22 KPVSLSYRCPCRFFESVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIQE 81

QY 25 YLEKALN 31
 Db 82 YLEKALN 88

RESULT 6
 Sequence 421, Application US/09312283C
 Patent No. 6573095
 GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James G.
 APPLICANT: Kumbla, Krishanand D.
 TITLE OF INVENTION: Compositions Isolated from Skin Cells
 TITLE OF INVENTION: and Methods for Their Use
 FILE REFERENCE: 11000.101c2
 CURRENT APPLICATION NUMBER: US/09/312, 283C
 CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 425
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 421
 LENGTH: 93
 TYPE: PRT
 ORGANISM: Mouse
 ; US-09-312-283C-421

Query Match 66.9%; Score 117; DB 4; Length 93;
 Best Local Similarity 40.3%; Pred. No. 6.9e-09; 0; Mismatches 4; Indels 36; Gaps 1;
 Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;

QY 1 KPVSLSYRCPCRFFGG-----GGLKWIQE 24
 Db 22 KPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIQE 81

QY 25 YLEKALN 31
 Db 82 YLEKALN 88

RESULT 7
 Sequence 5, Application US/09646028
 Patent No. 6562347
 GENERAL INFORMATION:
 APPLICANT: Kwak, Larry
 APPLICANT: Biragyn, Arya
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
 TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
 FILE REFERENCE: 14014.0316/P
 CURRENT APPLICATION NUMBER: US/09/646, 028
 CURRENT FILING DATE: 2000-09-12
 PRIOR APPLICATION NUMBER: 60/077, 745
 PRIOR FILING DATE: 1998-03-12
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 166
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-5

SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/835-107a-11
 FILING DATE:
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne
 REGISTRATION NUMBER: P-41,323
 REFERENCE/DOCKET NUMBER: GI5291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein

RESULT 8

US-09-646-028-54

; Sequence 54, Application US/09646028

; Patent No. 6552347

; GENERAL INFORMATION:

; APPLICANT: Kwak, Larry

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

; FILE REFERENCE: 14014.0316/P

; CURRENT APPLICATION NUMBER: US/09/646, 028

; CURRENT FILING DATE: 2000-09-12

; PRIOR APPLICATION NUMBER: 60/077, 745

; PRIOR FILING DATE: 1998-03-12

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 54

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-09-646-028-54

RESULT 10

US-08-808-720-1

; Sequence 1, Application US/08808720

; Patent No. 6100387

; GENERAL INFORMATION:

; APPLICANT: Herrmann, Steve

; TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING

; TITLE OF INVENTION: CHEMOKINE DOMAINS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; STREET: 87 CambridgePark

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/808,720

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne

; REGISTRATION NUMBER: P-41,323

; REFERENCE/DOCKET NUMBER: GI5291

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 328 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein
; US-08-808-720-1
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-221-013A-8
; Query Match 66.9%; Score 117; DB 3; Length 328;
; Best Local Similarity 40.3%; Pred. No. 2.5e-08;
; Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPARTN: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646, 028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence;/note=synthetic construct
; US-09-646-028-55
; Query Match 66.9%; Score 117; DB 4; Length 339;
; Best Local Similarity 40.3%; Pred. No. 2.6e-08;
; Matches 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: YLEKALN 31
; APPARTN: YLEKALN 70
; DB
; RESULT 12
; US-09-221-013A-8
; Sequence 8, Application US/09221013A
; Patent No. 6495740
; GENERAL INFORMATION:
; APPLICANT: Arioli, Antonio
; APPARTN: Williamson, Richard E.
; APPLICANT: Betzner, Andreas S.
; APPLICANT: Peng, Liangcai
; TITLE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan
; FILE REFERENCE: 96-98
; CURRENT APPLICATION NUMBER: US/09/221,013A
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: PCT/AU97/00402
; PRIOR FILING DATE: 1997-06-24
; PRIOR APPLICATION NUMBER: AU P00699
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; Query Match 34.9%; Score 61; DB 4; Length 1084;
; Best Local Similarity 43.5%; Pred. No. 3.6;
; Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
; Sequence 6, Application US/08960048C
; Patent No. 6271443
; GENERAL INFORMATION:
; APPLICANT: Stalker, D. et al.
; TITLE OF INVENTION: Plant Cellulose Synthase and Promoter
; TITLE OF INVENTION: Sequences
; FILE REFERENCE: 15621/01/US
; CURRENT APPLICATION NUMBER: US/08/960, 048C
; CURRENT FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/029, 987
; PRIOR FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Gossypium hirsutum
; US-08-960-048-6
; Query Match 34.6%; Score 60.5; DB 3; Length 974;
; Best Local Similarity 54.5%; Pred. No. 3.8;
; Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
; Sequence 3, Application US/08960048C
; Patent No. 6271443
; GENERAL INFORMATION:
; APPLICANT: YLEKALN 31
; APPARTN: YLEKALN 70
; DB
; RESULT 14
; US-09-838-586-6
; Sequence 6, Application US/09838586
; Patent No. 6576818
; GENERAL INFORMATION:
; APPLICANT: Stalker, D. et al.
; TITLE OF INVENTION: Plant Cellulose Synthase and Promoter
; TITLE OF INVENTION: Sequences
; FILE REFERENCE: 15621/02/US
; CURRENT APPLICATION NUMBER: US/09/838, 586
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/029, 987
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 08/960, 048
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Gossypium hirsutum
; US-09-838-586-6
; Query Match 34.6%; Score 60.5; DB 4; Length 974;
; Best Local Similarity 54.5%; Pred. No. 3.8;
; Matches 12; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Db 721 IFLSRHCPPLWYGGGRKLWLQ 742

RESULT 15
US-09-252-991A-25662
Sequence 25662, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25662
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-25662

Query Match 33 1%; Score 58; DB 4; Length 535;
Best Local Similarity 43.3%; Pred. No. 4.6;
Matches 13; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PVSLSYRCPCRFGGGLKWIQEYLEKALN 31
| || | : | || | || |
Db 265 PYPYDYRCPPGLGGEAGVKANLHYLENLLN 294

Search completed: October 9, 2003, 09:22:07
Job time : 30 secs

Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 09:18:21 ; Search time 375 Seconds
(Without alignments)
13.320 Million cell updates/sec

Title: US-09-835-107A-11
Perfect score: 1 KPVSLSYRCPCREFGGGLKWIQEYLEKALN 31
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 600653
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_NNEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/us10_NEW_PUB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/us60_NNEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/us60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/us60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	175	100.0	31	Sequence 13, Appl
2	175	100.0	31	Sequence 15, Appl
3	175	100.0	31	Sequence 20, Appl
4	175	100.0	31	Sequence 21, Appl
5	175	100.0	31	Sequence 22, Appl
6	175	100.0	31	Sequence 23, Appl
7	175	100.0	31	Sequence 26, Appl
8	175	100.0	31	Sequence 27, Appl
9	175	100.0	31	Sequence 13, Appl
10	175	100.0	31	Sequence 15, Appl
11	175	100.0	31	Sequence 20, Appl
12	175	100.0	31	Sequence 21, Appl
13	175	100.0	31	Sequence 22, Appl
14	175	100.0	31	Sequence 23, Appl
15	100.0	31	Sequence 26, Appl	

ALIGNMENTS

RESULT 1
US-09-835-107-13
Sequence 13, Application US/09835107
Patent No. US2002016512A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (16)-(19)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3 OTHER INFORMATION: or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory;
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
SEQUENCE: ; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
US-09-835-107-13

Query Match 100.0%; Score 175; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-09-835-107-15
 ; Sequence 15, Application US/09835107
 ; Patent No. US20020165123A1

; GENERAL INFORMATION:
 ; APPLICANT: Tudan, Christopher R.
 ; APPLICANT: Merzouk, Ahmed
 ; APPLICANT: Arab, Lakhdar
 ; APPLICANT: Salari, Hassan
 ; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
 ; FILE REFERENCE: SMAR012
 ; CURRENT APPLICATION NUMBER: US/09/835,107
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: CA 2,305,036
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/232,425
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: CA 2,335,109
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SEQ ID NO 20
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (15)..(18)
 ; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
 ; CURRENT APPLICATION NUMBER: US/09/835,107
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: CA 2,305,036
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/232,425
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: CA 2,335,109
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (15)..(18)
 ; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
 ; CURRENT APPLICATION NUMBER: US/09/835,107
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: CA 2,305,036
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/232,425
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: CA 2,335,109
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SEQ ID NO 20
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (24)..(28)
 ; OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
 ; CURRENT APPLICATION NUMBER: US/09/835,107
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: CA 2,305,036
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/232,425
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: CA 2,335,109
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (15)..(18)
 ; OTHER INFORMATION: spacer monomers (such as the illustrated glycine
 ; CURRENT APPLICATION NUMBER: US/09/835,107
 ; CURRENT FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: CA 2,305,036
 ; PRIOR FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/232,425
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: CA 2,335,109
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 34
 ; SEQ ID NO 20
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (15)..(18)

RESULT 3
 US-09-835-107-20
 ; Sequence 20, Application US/09835107
 ; Patent No. US20020165123A1

; GENERAL INFORMATION:
 ; APPLICANT: Tudan, Christopher R.
 ; APPLICANT: Merzouk, Ahmed
 ; APPLICANT: Arab, Lakhdar
 ; APPLICANT: Salari, Hassan
 ; APPLICANT: Eaves, Connie J.
 ; APPLICANT: Cashman, Johanne
 ; APPLICANT: Clark-Lewis

QY 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31
 Db 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31

Query Match 100.0%; Score 175; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-09-835-107-21
 ; Sequence 21, Application US/09835107
 ; Patent No. US20020165123A1

; GENERAL INFORMATION:
 ; APPLICANT: Tudan, Christopher R.
 ; APPLICANT: Merzouk, Ahmed
 ; APPLICANT: Arab, Lakhdar
 ; APPLICANT: Salari, Hassan
 ; APPLICANT: Eaves, Connie J.
 ; APPLICANT: Clark-Lewis

QY 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31
 Db 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31

Query Match 100.0%; Score 175; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-09-835-107-22
 ; Sequence 22, Application US/09835107
 ; Patent No. US20020165123A1

; GENERAL INFORMATION:
 ; APPLICANT: Tudan, Christopher R.
 ; APPLICANT: Merzouk, Ahmed
 ; APPLICANT: Arab, Lakhdar
 ; APPLICANT: Salari, Hassan
 ; APPLICANT: Eaves, Connie J.
 ; APPLICANT: Cashman, Johanne
 ; APPLICANT: Clark-Lewis

QY 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31
 Db 1 KPVSLSYRCPCRFGGGLKWIQUEYLEKALN 31

OTHER INFORMATION: spacer monomers (such as the illustrated glycine (G's) may be used in variable numbers, such as 2, 3 OTHER INFORMATION: or 4 glycines.

NAME/KEY: DOMAIN
LOCATION: (20).:(24)

OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K) residues may be joined by side chain cyclization

OTHER INFORMATION: using a lactam formation.

OTHER INFORMATION: Synthesised in Laboratory:

; OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid
; US-09-835-107-21

Query Match ; Best Local Similarity 100.0%; Pred. No. 4.9e-17; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 5
US-09-835-107-22

; Sequence 22, Application US/09835107
; Patent No. US20020165123A1

GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis

; APPLICANT: Salari, Hassan

TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: SMAR012

CURRENT APPLICATION NUMBER: US/09/835,107

PRIOR APPLICATION NUMBER: CA 2, 305, 036

PRIOR FILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: US 60/232,425

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: CA 2, 335, 109

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 23

LENGTH: 31

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: DOMAIN
LOCATION: (15).:(18)

OTHER INFORMATION: spacer monomers (such as the illustrated glycine (G's) may be used in variable numbers, such as 2, 3 OTHER INFORMATION: or 4 glycines.

NAME/KEY: DOMAIN
LOCATION: (20).:(24)

OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K) residues may be joined by side chain cyclization using a lactam formation procedure.

OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid

NAME/KEY: MOD_RES
LOCATION: (31)

OTHER INFORMATION: amide: or CTCE0021

LOCATION: (31)

OTHER INFORMATION: AMIDATION

US-09-835-107-23

Query Match ; Best Local Similarity 100.0%; Pred. No. 4.9e-17; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 6
US-09-835-107-23

; Sequence 23, Application US/09835107
; Patent No. US20020165123A1

GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Query Match ; Best Local Similarity 100.0%; Pred. No. 4.9e-17; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 7
US-09-835-107-26

; Sequence 26, Application US/09835107
; Patent No. US20020165123A1

GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Arab, Lakhdar

; APPLICANT: Saxena, Geeta

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31
Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Query Match ; Best Local Similarity 100.0%; Pred. No. 4.9e-17; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid
; US-10-086-177A-20

Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Indels	Gaps	Mismatches
QY	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN	31	31;	100.0%	4.9e-17;	0;	0;	0;	0;
Db	1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN	31							

RESULT 12
US-10-086-177A-21

Sequence	Publication No.	GENERAL INFORMATION:
21, Application US/10086177A	US20030148940A1	

; Sequence 21, Application US/10086177A
; Publication No. US20030148940A1

; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis, Ian

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: Cells

; FILE REFERENCE: SMAR-012CIP

; CURRENT APPLICATION NUMBER: US/10/086,177A

; PRIOR FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 60/232,425

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: CA 2,305,036

; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: CA 2,335,109

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)

; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (55-67) amide: or CTC0017

; US-10-086-177A-15

Query Match 100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17; Mismatches 0;
Matches 31; Conservative 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 11
US-10-086-177A-20

; Sequence 20, Application US/10086177A

; Publication No. US20030148940A1

; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis, Ian

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic

; FILE REFERENCE: SMAR-012CIP

; CURRENT APPLICATION NUMBER: US/10/086,177A

; PRIOR FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 60/232,425

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: 60/232,425

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: CA 2,305,036

; PRIOR FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: CA 2,335,109

; PRIOR FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)

; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (55-67) - K20/E24-cyclic acid

; US-10-086-177A-21

Query Match 100.0%; Score 175; DB 12; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-17; Mismatches 0;
Matches 31; Conservative 0; Indels 0; Gaps 0;

QY 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

Db 1 KPVSLSYRCPCRFGGGLKWIQEYLEKALN 31

RESULT 13
US-10-086-177A-22

; Sequence 22, Application US/10086177A

; Publication No. US20030148940A1

; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.

; APPLICANT: Merzouk, Ahmed

; APPLICANT: Salari, Hassan

; APPLICANT: Eaves, Connie J.

; APPLICANT: Cashman, Johanne

; APPLICANT: Clark-Lewis, Ian

; APPLICANT: Salari, Hassan

; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic

; FILE REFERENCE: SMAR-012CIP

; CURRENT APPLICATION NUMBER: US/10/086,177A

CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic acid: or CTCE0022
; US-10-086-177A-22

Query Match 100.0%; Score 175; DB 12; Length 31;
; Best Local Similarity 100.0%; Pred. No. 4.9e-17;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31
; Db 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31

RESULT 14
; US-10-086-177A-23
; Sequence 23, Application US/10086177A
; Publication No. US20030148940A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
; FILE REFERENCE: SMAR-012CIP
; CURRENT APPLICATION NUMBER: US/10/086,177A
; PRIOR APPLICATION NUMBER: 09/835,107
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/232,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRICE APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
; US-10-086-177A-26

Query Match 100.0%; Score 175; DB 12; Length 31;
; Best Local Similarity 100.0%; Pred. No. 4.9e-17;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31
; Db 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31

Search completed: October 9, 2003, 09:28:28
; Job time : 375 secs

Query Match 100.0%; Score 175; DB 12; Length 31;
; Best Local Similarity 100.0%; Pred. No. 4.9e-17;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31
; Db 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31

Query Match 100.0%; Score 175; DB 12; Length 31;
; Best Local Similarity 100.0%; Pred. No. 4.9e-17;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31
; Db 1 KPVSLSYRCPCCRFFGGGLKWIQEYLEKALN 31